

-120 -100 -80  
BgIII PvuII

AAGCTCAGATCTACCTGCCTGAGGGCGTCCGGTTCCAGCTGGCCCTTOCCGAGGGGGAGA

-60 -40 -20

GGGAGGCGTTTCTAAAAGCCCTTCAGGACGCTACCCGGGGGCGGGTGGTGGAAGGGTAAC

1 20 40 60

ATGAGGGGGATGCTGCCCCCTCTTTGAGCCCAAGGGCCGGGTCCTCCTGGTGGACGGCCAC  
MetArgGlyMetLeuProLeuPheGluProLysGlyArgValLeuLeuValAspGlyHis

1

80 100 120

CACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCAGCCGGGGGAGCCG  
HisLeuAlaTyrArgThrPheHisAlaLeuLysGlyLeuThrThrSerArgGlyGluPro

140 160 180

GTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGGCCCTCAAGGAGGACGGGGAC  
ValGlnAlaValTyrGlyPheAlaLysSerLeuLeuLysAlaLeuLysGluAspGlyAsp

41

200 220 240

GCGGTGATCGTGGTCTTTGACCCAAGGCCCTCCTTCCGCCACGAGGCCTACGGGGGG  
AlaValIleValValPheAspAlaLysAlaProSerPheArgHisGluAlaTyrGlyGly

260 280 300

TACAAGGCGGGCCGGGGCCCCACGCCGGAGGACTTTCCC CGCAACTCGCCCTCATCAAG  
TyrLysAlaGlyArgAlaProThrProGluAspPheProArgGlnLeuAlaLeuIleLys

81

320 340 360

XhoI

GAGCTGGTGGACCTCCTGGGGCTGGCGCGCCTCGAGGTCCC GGGCTACGAGGCGGACGAC  
GluLeuValAspLeuLeuGlyLeuAlaArgLeuGluValProGlyTyrGluAlaAspAsp

## FIGURE 1

## TAQ DNA POLYMERASE SEQUENCE

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380	400	420
GTCCTGGCCAGCCTGGCCAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCCTCACC		
ValLeuAlaSerLeuAlaLysLysAlaGluLysGluGlyTyrGluValArgIleLeuThr		
121		
440	460	480
GCCGACAAAGACCTTTACCAGCTCCTTTCCGACCGCATCCACGTCCTCCACCCCGAGGGG		
AlaAspLysAspLeuTyrGlnLeuLeuSerAspArgIleHisValLeuHisProGluGly		
500	520	540
Asp718		
TACCTCATCACCCCGGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCGACCAGTGGGCC		
TyrLeuIleThrProAlaTrpLeuTrpGluLysTyrGlyLeuArgProAspGlnTrpAla		
161		
560	580	600
GACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGGCATCGGG		
AspTyrArgAlaLeuThrGlyAspGluSerAspAsnLeuProGlyValLysGlyIleGly		
620	640	660
HindIII		
GAGAAGACGGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAGCCCTCCTCAAGAAC		
GluLysThrAlaArgLysLeuLeuGluGluTrpGlySerLeuGluAlaLeuLeuLysAsn		
201		
680	700	720
CTGGACCGGCTGAAGCCCGCCATCCGGGAGAAGATCCTGGCCACATGGACGATCTGAAG		
LeuAspArgLeuLysProAlaIleArgGluLysIleLeuAlaHisMetAspAspLeuLys		
740	760	780
CTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCTGCCCCTGGAGGTGGACTTCGCCAAA		
LeuSerTrpAspLeuAlaLysValArgThrAspLeuProLeuGluValAspPheAlaLys		
241		
800	820	840
AGGCGGGAGCCCGACCGGGAGAGGCTTAGGGCCTTTCTGGAGAGGCTTGAGTTTGGCAGC		
ArgArgGluProAspArgGluArgLeuArgAlaPheLeuGluArgLeuGluPheGlySer		

FIGURE 1

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## TAQ DNA POLYMERASE SEQUENCE

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860 880 900  
*BstXI*  
CTCCTCCACGAGTTCGGCCTTCTGGAAAGCCCCAAGGCCCTGGAGGAGGCCCTGGCCC  
LeuLeuHisGluPheGlyLeuLeuGluSerProLysAlaLeuGluGluAlaProTrpPro  
281 290

920 940 960  
CCGCCGGAAGGGGCCTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGAT  
ProProGluGlyAlaPheValGlyPheValLeuSerArgLysGluProMetTrpAlaAsp

980 1000 1020  
CTTCTGGCCCTGGCCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAA  
LeuLeuAlaLeuAlaAlaAlaArgGlyGlyArgValHisArgAlaProGluProTyrLys  
321

1040 1060 1080  
GCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCC  
AlaLeuArgAspLeuLysGluAlaArgGlyLeuLeuAlaLysAspLeuSerValLeuAla

1100 1120 1140  
CTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTACCTCCTG  
LeuArgGluGlyLeuGlyLeuProProGlyAspAspProMetLeuLeuAlaTyrLeuLeu  
361

1160 1180 1200  
GACCCTTCCAACACCACCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGAGTGGACGGAG  
AspProSerAsnThrThrProGluGlyValAlaArgArgTyrGlyGlyGluTrpThrGlu

1220 1240 1260  
GAGGCGGGGGAGCGGGCCGCTTTCCGAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTT  
GluAlaGlyGluArgAlaAlaLeuSerGluArgLeuPheAlaAsnLeuTrpGlyArgLeu  
401

1280 1300 1320  
GAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAGGTGGAGAGGCCCTTTCCGCTGTC  
GluGlyGluGluArgLeuLeuTrpLeuTyrArgGluValGluArgProLeuSerAlaVal

## FIGURE 1

## TAQ DNA POLYMERASE SEQUENCE

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1340 1360 1380  
CTGGCCACATGGAGGCCACGGGGGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTC  
LeuAlaHisMetGluAlaThrGlyValArgLeuAspValAlaTyrLeuArgAlaLeuSer  
441

1400 1420 1440  
*XhoI*  
CTGGAGGTGGCCGAGGAGATCGCCCGCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCAC  
LeuGluValAlaGluGluIleAlaArgLeuGluAlaGluValPheArgLeuAlaGlyHis

1460 1480 1500  
*PvuII*  
CCCTTCAACCTCAACTCCCGGGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTT  
ProPheAsnLeuAsnSerArgAspGlnLeuGluArgValLeuPheAspGluLeuGlyLeu  
481

1520 1540 1560  
CCCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCGTCCTGGAG  
ProAlaIleGlyLysThrGluLysThrGlyLysArgSerThrSerAlaAlaValLeuGlu

1580 1600 1620  
*PstI* *SacI*  
GCCCTCCGCGAGGCCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAG  
AlaLeuArgGluAlaHisProIleValGluLysIleLeuGlnTyrArgGluLeuThrLys  
521

1640 1660 1680  
CTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCAGGACGGGCCGCTC  
LeuLysSerThrTyrIleAspProLeuProAspLeuIleHisProArgThrGlyArgLeu

1700 1720 1740  
CACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTCCGATCCCAAC  
HisThrArgPheAsnGlnThrAlaThrAlaThrGlyArgLeuSerSerSerAspProAsn  
561

1760 1780 1800  
*BamHI*  
CTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCGGGCCTTCATCGCC  
LeuGlnAsnIleProValArgThrProLeuGlyGlnArgIleArgArgAlaPheIleAla

## FIGURE 1

TAQ DNA POLYMERASE SEQUENCE  
5/6

1820 1840 1860  
*SacI*  
GAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGATAGAGCTCAGGGTGCTGGCC  
GluGluGlyTrpLeuLeuValAlaLeuAspTyrSerGlnIleGluLeuArgValLeuAla  
601

1880 1900 1920  
CACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTCCAGGAGGGGCGGGACATCCACAG  
HisLeuSerGlyAspGluAsnLeuIleArgValPheGlnGluGlyArgAspIleHisThr

1940 1960 1980  
*PvuII*  
GAGACCGCCAGCTGGATGTTTCGGCGTCCCCCGGGAGGCCGTGGACCCCCTGATGCGCCGG  
GluThrAlaSerTrpMetPheGlyValProArgGluAlaValAspProLeuMetArgArg  
641

2000 2020 2040  
GCGGCCAAGACCATCAACTTCGGGGTCTCTACGGCATGTTCGGCCCACCGCCTCTCCAG  
AlaAlaLysThrIleAsnPheGlyValLeuTyrGlyMetSerAlaHisArgLeuSerGln

2060 2080 2100  
*NheI*  
GAGCTAGCCATCCCTTACGAGGAGGCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTC  
GluLeuAlaIleProTyrGluGluAlaGlnAlaPheIleGluArgTyrPheGlnSerPhe  
681

2120 2140 2160  
CCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTG  
ProLysValArgAlaTrpIleGluLysThrLeuGluGluGlyArgArgArgGlyTyrVal

2180 2200 2220  
GAGACCCTCTTCGGCCGCCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGTG  
GluThrLeuPheGlyArgArgArgTyrValProAspLeuGluAlaArgValLysSerVal  
721

## TAQ DNA POLYMERASE SEQUENCE

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2240 2260 2280  
CGGGAGGCGGCGGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGCCGACCTC  
ArgGluAlaAlaGluArgMetAlaPheAsnMetProValGlnGlyThrAlaAlaAspLeu  
741

2300 2320 2340  
ATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGGCCAGGATGCTC  
MetLysLeuAlaMetValLysLeuPheProArgLeuGluGluMetGlyAlaArgMetLeu

2360 2380 2400  
*XhoI*  
CTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCAAAAGAGAGGGCGGAGGCCGTGGCC  
LeuGlnValHisAspGluLeuValLeuGluAlaProLysGluArgAlaGluAlaValAla  
781

2420 2440 2460  
CGGCTGGCCAAGGAGGTCATGGAGGGGGTSTATCCCTGGCCGTGCCCTGGAGGTGGAG  
ArgLeuAlaLysGluValMetGluGlyValTyrProLeuAlaValProLeuGluValGlu

2480 2500  
GTGGGGATAGGGGAGGACTGGCTCTCCGCCAAGGAGTGATACCACC  
ValGlyIleGlyGluAspTrpLeuSerAlaLysGluEnd  
821 832

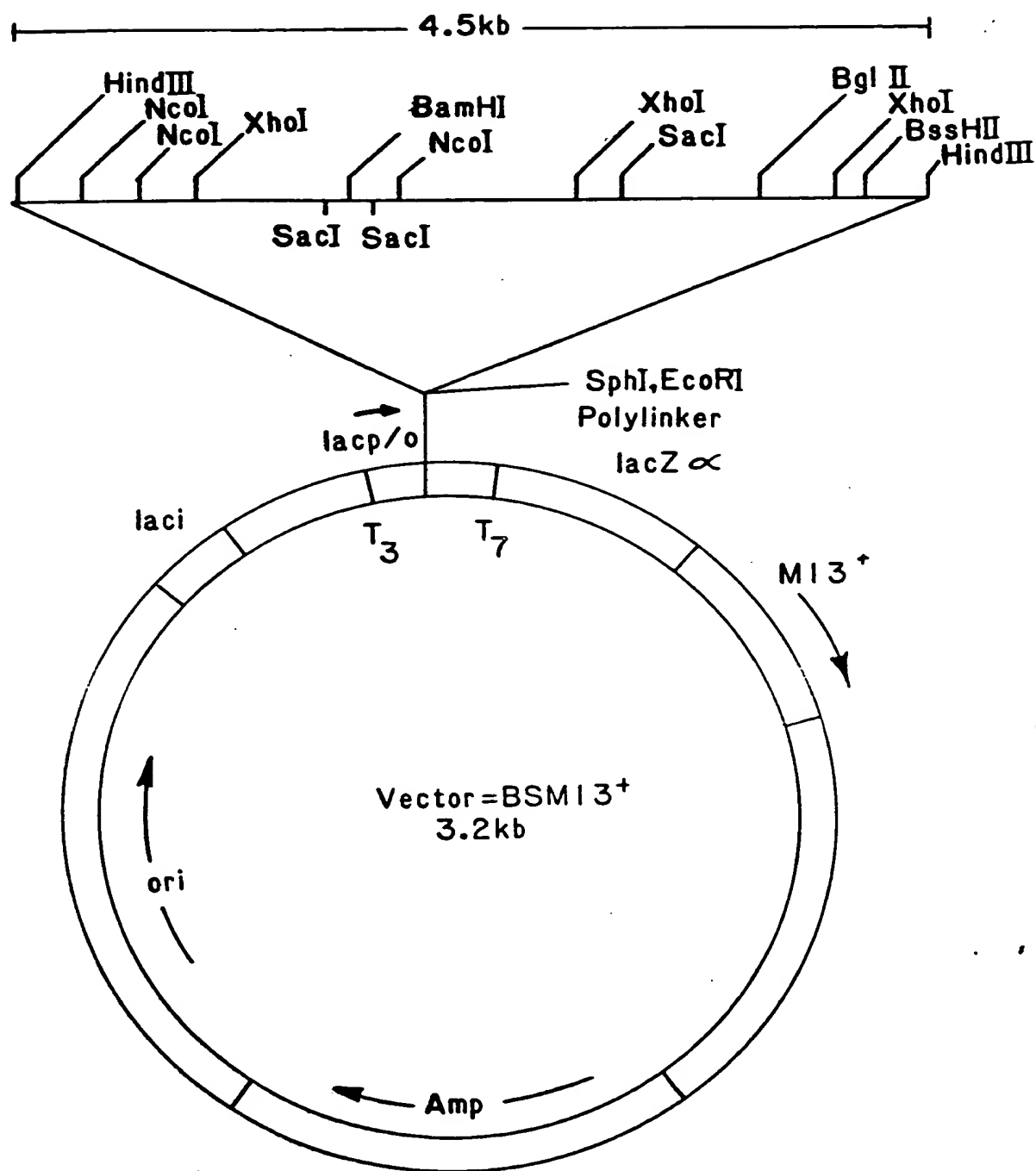


FIG. 2

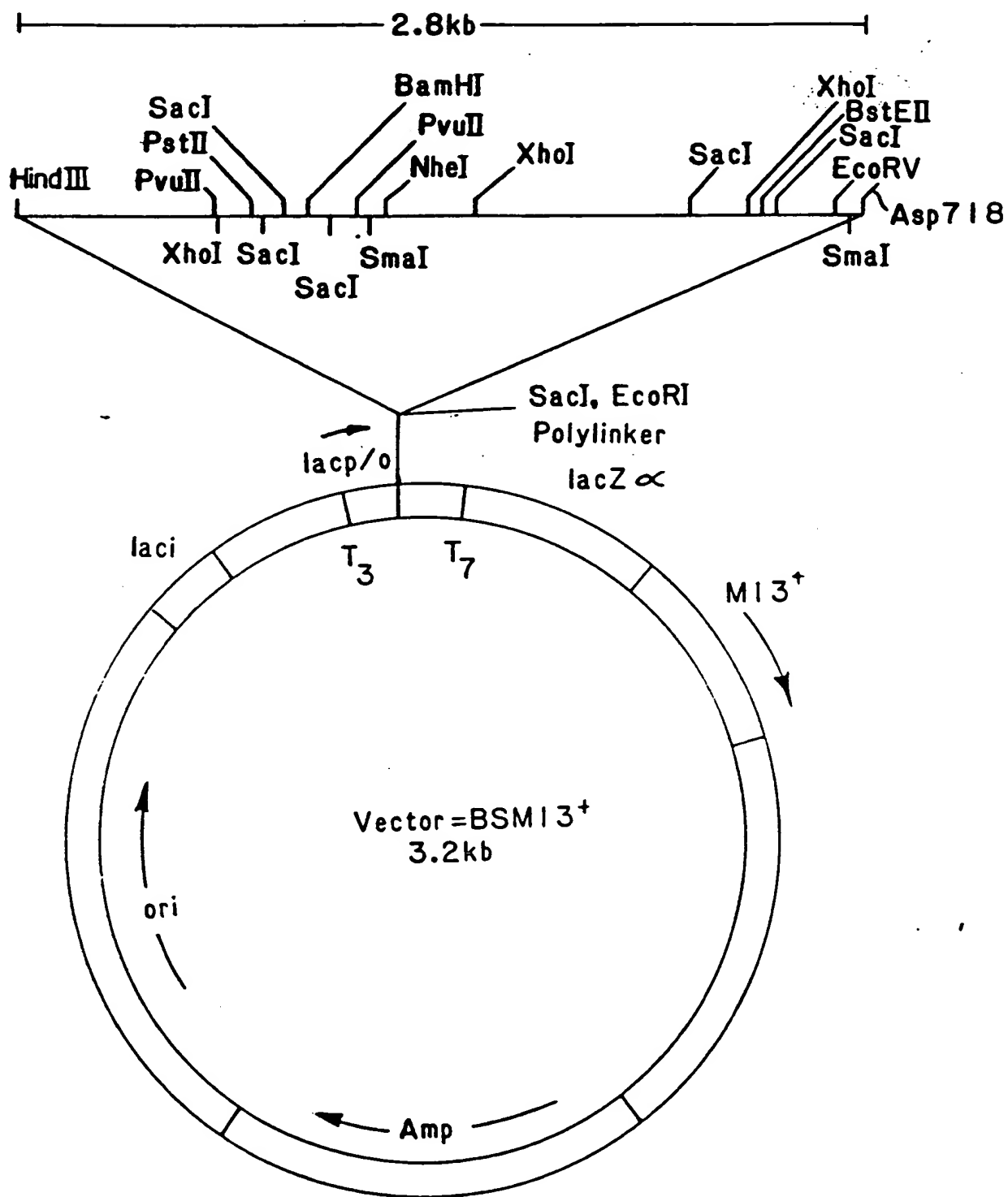


FIG. 3